

S1 Text: Modelling results

Comparative analysis of dengue and Zika outbreaks reveals differences by setting and virus
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Introduction

This document contains the R code necessary to reproduce the results in “Comparative analysis of dengue and Zika outbreaks reveals differences by setting and virus.” All code and data used here are in a github repository. The data sets for the three outbreaks are contained in the `data` subdirectory.

Required packages

```
cran_packages <- c("cowplot", "dplyr", "tidyverse", "stringi", "msm", "rbi")
github_packages <- c("sbfnk/RBi.helpers")

for (package in cran_packages) {
  install.packages(package)
}

library("devtools")

for (package in github_packages) {
  install_github(package)
}
```

Generate MCMC chains

Generating MCMC chains requires a working installation of libbi v1.2.0. The model code is in `vbd.bi`, which is run by the R script `dengue_zika_mcmc.r`.

Edit the lines starting `code_dir <-` and `output_dir <-` in the script ‘`dengue_zika_mcmc.r`’ from the R/ directory in the github repository to point to the correct directories, and run it using

```
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations
```

The first line runs with $D_{\text{life},M} = 2$ weeks, and the second one with $D_{\text{life},M} = 1$ week

Analyse MCMC chains

Set the `code_dir` and `output_dir` to the value used in `sample.posterior.r`

```
output_dir <- "insert your directory here"
code_dir <- "insert your directory here"
```

Load required packages

```

for (package in c(cran_packages, github_packages)) {
  library(tolower(sub("^.*/", "", package)), character.only = TRUE)
}

```

Load script from github repository (add path if necessary)

```
source(paste0(code_dir, "/R/", "analyse_traces.r"))
```

Get MCMC chains of the two libbi runs.

```
libbi_results <- analyse_traces(c("vbd_fnh", "vbd_fnh_shorter"), output_dir)
```

Calculate DIC for models with different mosquito life times (1 week vs. 2 weeks vs. both with equal probability)

```

dic <- sapply(libbi_results, function(x) {
  compute_DIC(x[["trace"]][[["posterior"]]])
})
dic

```

```

##           vbd_fnh vbd_fnh_shorter      vbd_fnh_all
##           366.7032       365.8579       366.2954

```

Plots

Prepare data

```

ts <- list()
analyses <- data.frame(setting = c("yap", "yap", "fais"), disease = c("dengue",
  "zika", "dengue"))

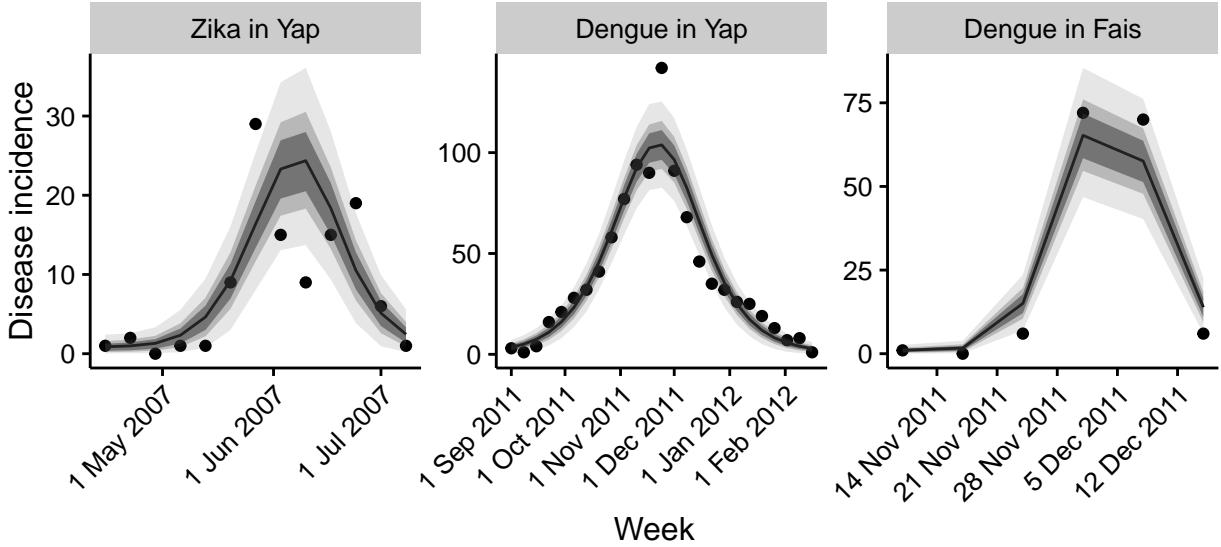
for (i in 1:nrow(analyses)) {
  this_setting <- analyses[i, "setting"]
  this_disease <- analyses[i, "disease"]
  this_filename <- paste(code_dir, "data", paste(this_setting, this_disease,
    "data.rds", sep = "_"), sep = "/")
  this_ts <- readRDS(this_filename) %>% mutate(setting = this_setting, disease = this_disease,
    week = floor(nr/7))
  ts <- c(ts, list(this_ts))
}

ordered_obs_id_levels <- c("yap_zika", "yap_dengue", "fais_dengue")

data_labels <- ordered_obs_id_levels
data_labels <- sub("(.*)(.*$)", "\\2 \\\1", data_labels)
data_labels <- sub(" ", " in ", stri_trans_totitle(data_labels))
names(data_labels) <- ordered_obs_id_levels

data <- bind_rows(ts) %>% group_by(week, setting, disease) %>% summarize(value = sum(value),
  onset_date = min(onset_date)) %>% ungroup() %>% mutate(obs_id = factor(paste(setting,
  disease, sep = "_"), levels = ordered_obs_id_levels, labels = data_labels)) %>%
  arrange(week, obs_id) %>% select(week, obs_id, value, onset_date) %>% rename(time = week) %>%
  mutate(state = "Cases")
first_obs <- data %>% group_by(obs_id) %>% filter(value > 0) %>% slice(which.min(time)) %>%
  select(time, obs_id) %>% rename(first_obs = time)

```



```
last_obs <- data %>% group_by(obs_id) %>% filter(value > 0) %>% slice(which.max(time)) %>%
  select(time, obs_id) %>% rename(last_obs = time)
data <- data %>% left_join(first_obs, by = "obs_id") %>% left_join(last_obs,
  by = "obs_id") %>% filter(time >= first_obs & time <= last_obs)
```

Fits

```
libbi_results[["vbd_fnh_all"]][["trace"]][["posterior"]][["Cases"]] <- libbi_results[["vbd_fnh_all"]][[["vbd_fnh_all"]]][["trace"]][["posterior"]][["Cases"]]
  mutate(obs_id = factor(obs_id, levels = ordered_obs_id_levels, labels = data_labels))
temp_plot <- plot_libbi(read = libbi_results[["vbd_fnh_all"]][["trace"]][["posterior"]][["Cases"]],
  model = libbi_results[["vbd_fnh_all"]][["model"]], data = data %>% filter(value >
    0), density_args = list(adjust = 2), extra.aes = list(group = "obs_id"),
  data.colour = "black", states = "Cases", trend = "mean", plot = FALSE, limit.to.data = TRUE,
  quantiles = c(0.5, 0.72, 0.95))
obs_states <- temp_plot$data$states %>% inner_join(data %>% select(time, obs_id,
  onset_date), by = c("time", "obs_id"))
p_obs <- ggplot(obs_states, aes(x = onset_date)) + geom_point(data = data, mapping = aes(y = value)) +
  facet_wrap(~obs_id, scales = "free") + scale_x_date("Week", labels = scales::date_format("%e %b %Y"),
  theme_cowplot(font_size = 12) + theme(axis.text.x = element_text(angle = 45,
  hjust = 1)) + facet_wrap(~obs_id, scales = "free") + scale_y_continuous("Disease incidence") +
  geom_line(aes(y = value)) + geom_ribbon(aes(ymin = min.1, ymax = max.1),
  alpha = 0.5) + geom_ribbon(aes(ymin = min.2, ymax = max.2), alpha = 0.25) +
  geom_ribbon(aes(ymin = min.3, ymax = max.3), alpha = 0.125)
p_obs
```

Other plots

Define plot labels

```
labels <- c(p_d_inc_h = "italic(D)[plain(inc,H)]", p_d_inc_m = "italic(D)[plain(inc,M)]",
  p_d_inf_h = "italic(D)[plain(inf,H)]", p_lm = "log[10](italic(m))", p_initial_susceptible_yap = "italic(m0)[plain(susceptible,YAP)]")
```

```

p_rep = "italic(r)", p_b_h = "italic(b)[H]", p_b_m = "italic(b)[M]", p_t_start = "italic(t[0])",
p_pop_yap = "italic(rho)", p_red_foi_yap = "italic(sigma)", p_p_patch_yap = "italic(phi)",
R0 = "italic(R)[H %->% H]", GI = "italic(G)", zika = "Zika", yap = "Yap",
fais = "Fais")

```

Marginal posterior densities

```

p <- plot_libbi(read = libbi_results[["vbd_fnh_all"]][["trace"]][["posterior"]],
prior = libbi_results[["vbd_fnh_all"]][["trace"]][["prior"]], model = libbi_results[["vbd_fnh_all"]],
density_args = list(bins = 20, alpha = 0.5, color = "black"), densities = "histogram",
extra.aes = list(color = "disease", linetype = "setting"), trend = "median",
plot = FALSE, quantiles = c(0.5, 0.95), labels = labels, brewer.palette = "Set1")
p$densities

```

Human-to-human reproduction number vs generation interval

```

temp_plot <- plot_libbi(read = libbi_results[["vbd_fnh_all"]][["trace"]][["posterior"]],
prior = libbi_results[["vbd_fnh_all"]][["trace"]][["prior"]], model = libbi_results[["vbd_fnh_all"]],
extra.aes = list(color = "disease", linetype = "setting", group = "p_d_life_m"),
plot = FALSE, labels = labels, states = c(), params = c("R0", "GI"), noises = c())

r0gi <- temp_plot$data$params %>% filter(distribution == "posterior") %>% mutate(obs_id = tolower(paste
disease, sep = " _")) %>% filter(obs_id != "fais_zika") %>% mutate(obs_id = factor(obs_id,
levels = ordered_obs_id_levels, labels = data_labels)) %>% spread(parameter,
value)

cross_sections <- data.frame(GI = c(3, 4))
colnames(cross_sections) <- "italic(G)"

p_r0vgi <- ggplot(r0gi, aes(x = `italic(G)` * 7)) + geom_jitter(aes(y = `italic(R)[H %->% H]`),
color = factor(p_d_life_m)) + facet_grid(~obs_id) + scale_x_continuous("Equilibrium generation interval",
scale_y_continuous(expression(italic(R)[H %->% H])) + scale_color_brewer("Mosquito life span",
palette = "Dark2", labels = c("1 week", "2 weeks")) + theme_cowplot(font_size = 12) +
theme(legend.position = "top") + facet_wrap(~obs_id, scales = "free") +
geom_rect(data = cross_sections, aes(xmin = `italic(G)` * 7 - 1, xmax = `italic(G)` *
7 + 1), ymin = -Inf, ymax = Inf, alpha = 0.2, lwd = 3)
p_r0vgi

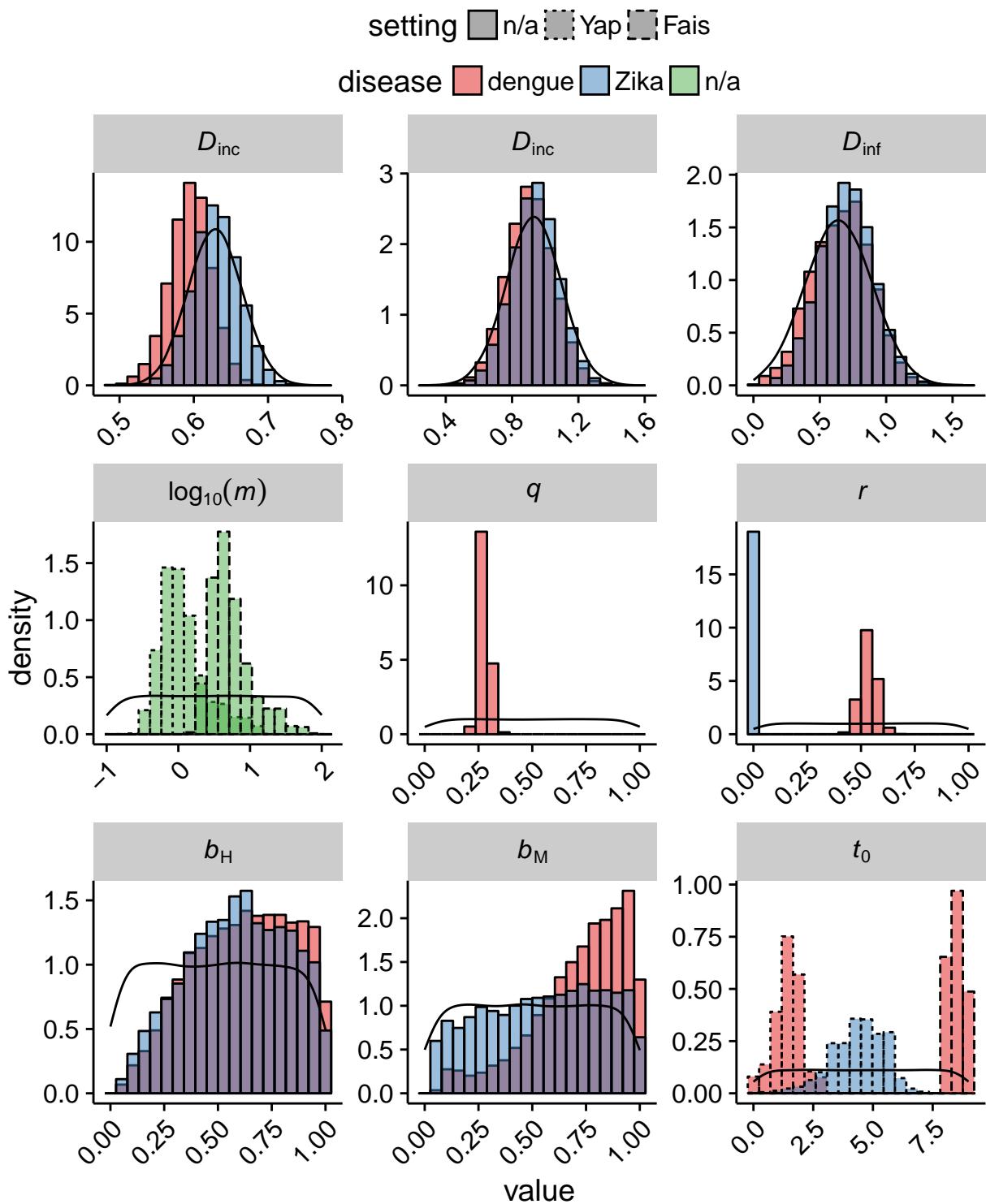
ggsave("r0vgi.pdf", p_r0vgi, height = 4, width = 8)

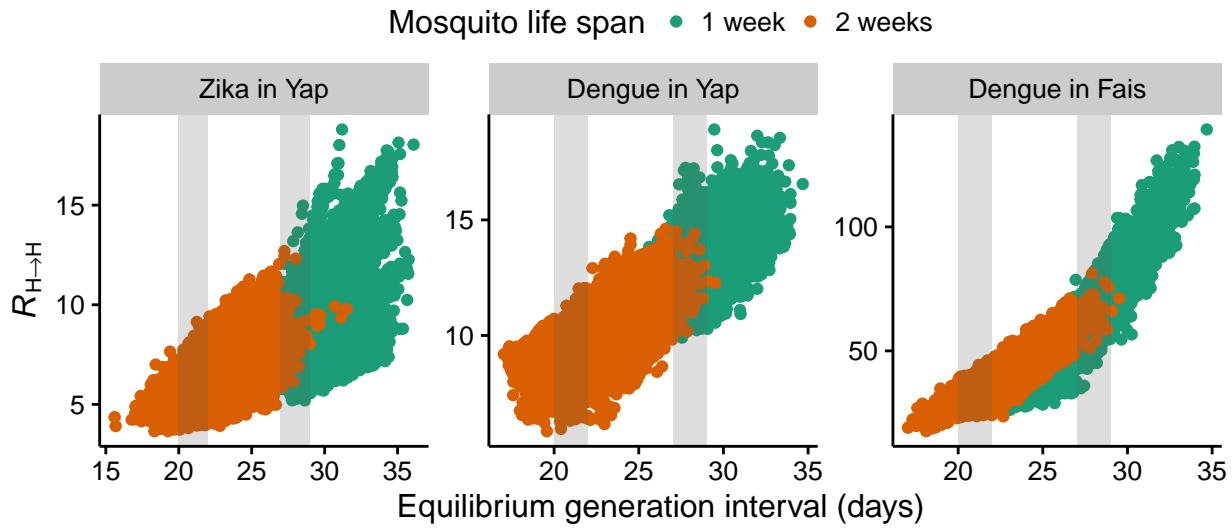
quantile_probs <- c(0.5, 0.25, 0.75, 0.025, 0.975)

r0gi %>% filter(abs(`italic(G)` - round(`italic(G)`)) <= 1/7) %>% mutate(GI = round(`italic(G)`)) %>%
filter(GI %in% c(3, 4)) %>% group_by(disease, setting, GI) %>% do(data.frame(prob = factor(quantile,
levels = quantile_probs), value = quantile(.`italic(R)[H %->% H]`, quantile_probs))) %>%
spread(prob, value)

## Source: local data frame [6 x 8]
## Groups: disease, setting, GI [6]
##
##   disease setting     GI     `0.5`    `0.25`    `0.75`    `0.025`    `0.975`

```





```
## * <fctr> <fctr> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 dengue     Yap     3 8.999201 8.428373 9.629400 7.387527 10.919147
## 2 dengue     Yap     4 12.830719 12.062139 13.597201 10.930578 15.070461
## 3 dengue     Fais    3 34.223608 31.457547 36.803482 26.510776 41.976421
## 4 dengue     Fais    4 65.443681 59.951370 71.269573 49.981494 81.281378
## 5   Zika     Yap     3 5.751687 5.272321 6.375527 4.359961 7.653887
## 6   Zika     Yap     4 8.432057 7.541383 9.670550 6.183408 11.746451
```

Traces

```
p$traces
```

Other models

These are the alternative models considered and mentioned in the manuscript.

Reduced population size in Yap

Generate MCMC chains

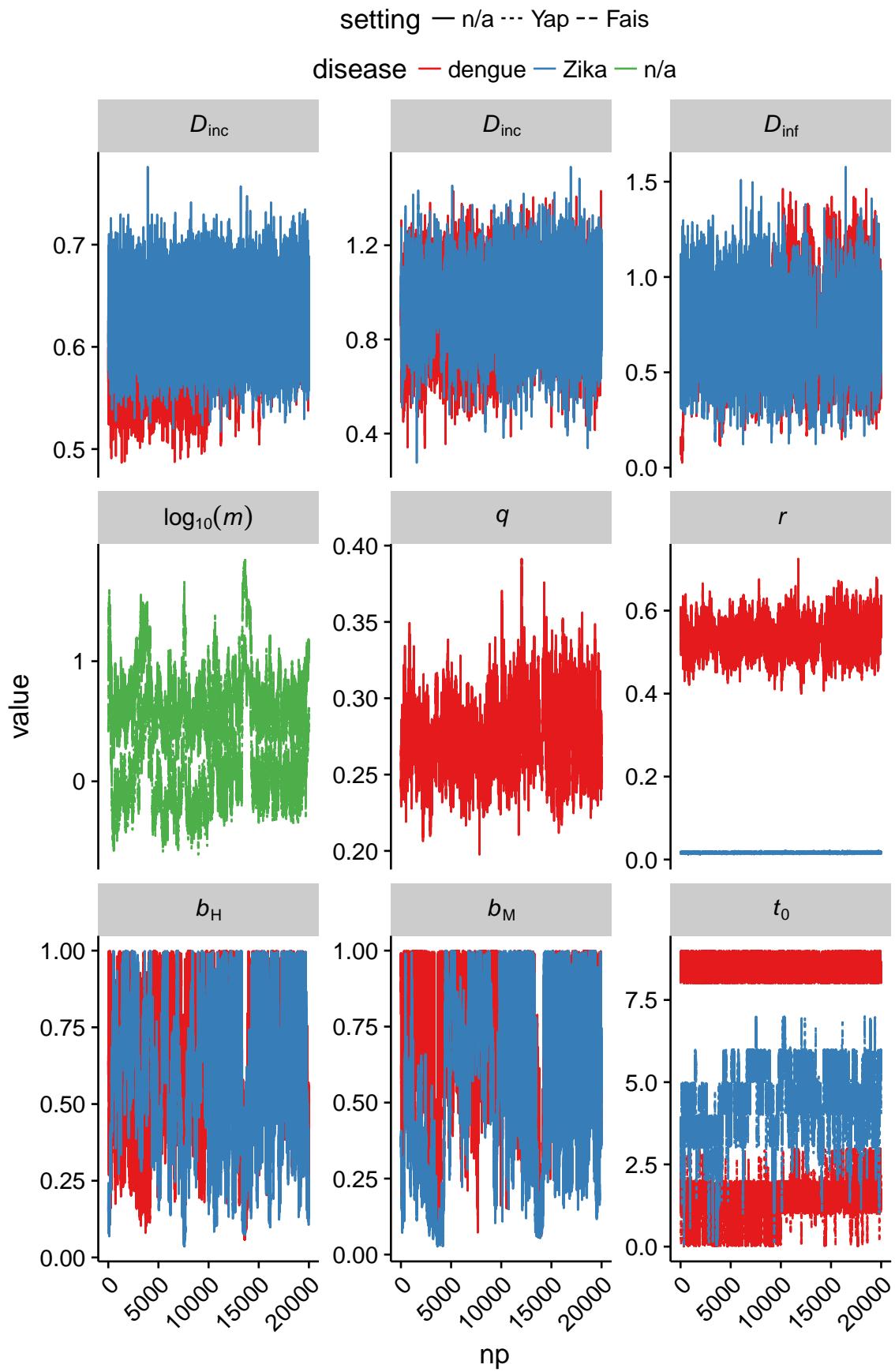
In this model, the population in Yap is reduced by a factor ρ .

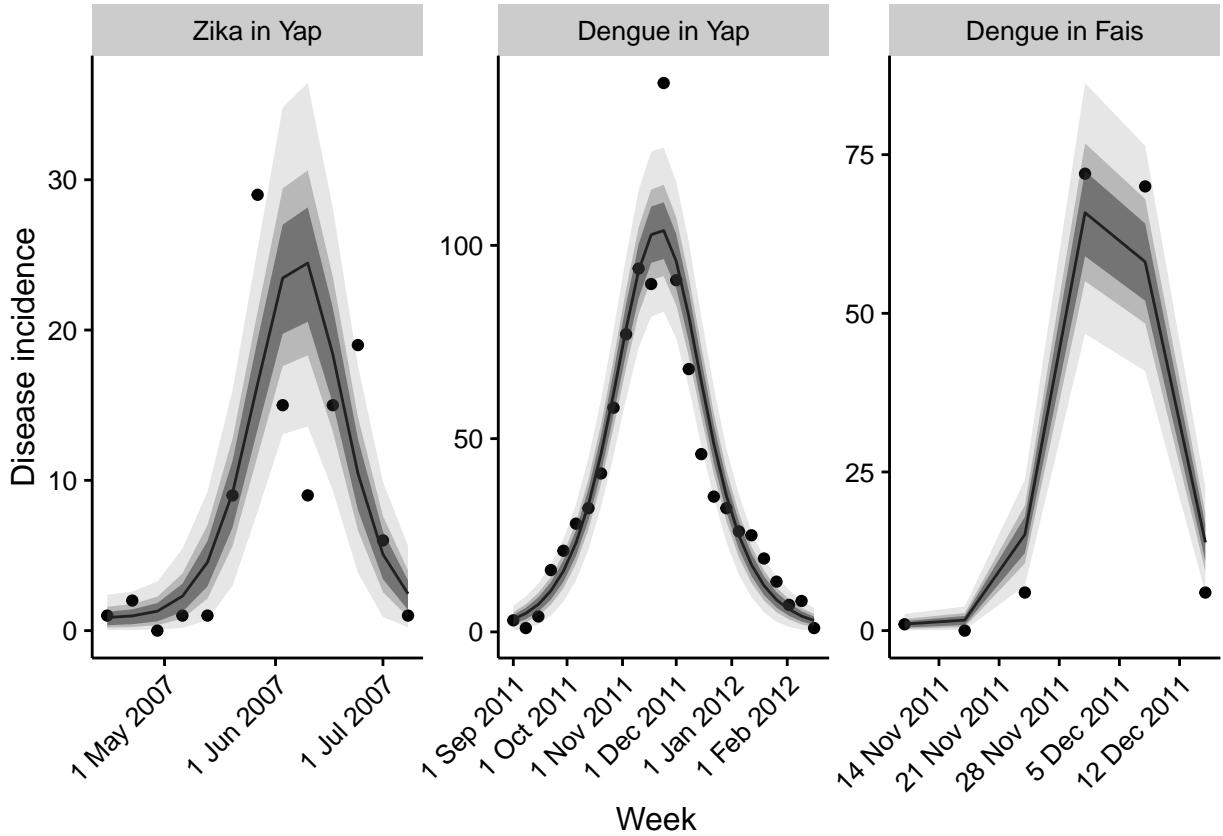
Fit the model (remember to update `code_dir` and `data_dir` in `dengue_zika_mcmc.r`):

```
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations
```

Get MCMC chains of the two libbi runs.

```
libbi_results <- analyse_traces(c("vbd_seropop_fnh", "vbd_seropop_fnh_shorter"),
                                output_dir)
```





Fits

```
libbi_results[["vbd_seropop_fnh_all"]][["trace"]][["posterior"]][["Cases"]] <- libbi_results[["vbd_seropop_fnh_all"]]
  mutate(obs_id = factor(obs_id, levels = ordered_obs_id_levels, labels = data_labels))
temp_plot <- plot_libbi(read = libbi_results[["vbd_seropop_fnh_all"]][["trace"]][["posterior"]][["Cases"]])
model = libbi_results[["vbd_seropop_fnh_all"]][["model"]], data = data %>%
  filter(value > 0), density_args = list(adjust = 2), extra.aes = list(group = "obs_id"),
  data.colour = "black", states = "Cases", trend = "mean", plot = FALSE, limit.to.data = TRUE,
  quantiles = c(0.5, 0.72, 0.95))
obs_states <- temp_plot$data$states %>% inner_join(data %>% select(time, obs_id,
  onset_date), by = c("time", "obs_id"))
p_obs <- ggplot(obs_states, aes(x = onset_date)) + geom_point(data = data, mapping = aes(y = value)) +
  facet_wrap(~obs_id, scales = "free") + scale_x_date("Week", labels = scales::date_format("%e %b %Y"))
  theme_cowplot(font_size = 12) + theme(axis.text.x = element_text(angle = 45,
  hjust = 1)) + facet_wrap(~obs_id, scales = "free") + scale_y_continuous("Disease incidence") +
  geom_line(aes(y = value)) + geom_ribbon(aes(ymin = min.1, ymax = max.1),
  alpha = 0.5) + geom_ribbon(aes(ymin = min.2, ymax = max.2), alpha = 0.25) +
  geom_ribbon(aes(ymin = min.3, ymax = max.3), alpha = 0.125)
p_obs
```

Marginal posterior densities

```

p <- plot_libbi(read = libbi_results[["vbd_sero_pop_fnh_all"]][["trace"]][["posterior"]],
                 prior = libbi_results[["vbd_sero_pop_fnh_all"]][["trace"]][["prior"]], model = libbi_results[["vbd_sero_fnh_all"]][["model"]],
                 density_args = list(bins = 20, alpha = 0.5, color = "black"), densities = "histogram",
                 extra.aes = list(color = "disease", linetype = "setting"), trend = "median",
                 plot = FALSE, quantiles = c(0.5, 0.95), labels = labels, brewer.palette = "Set1")
p$densities

```

Estimated final size for Zika in Yap (proportion infected in the outbreak)

```

n_infected <- libbi_results[["vbd_sero_pop_fnh_all"]][["trace"]][["posterior"]][["final_size"]] %>%
  filter(obs_id == "yap_zika") %>% .$value %>% quantile(c(0.025, 0.5, 0.975))
N <- libbi_results[["vbd_sero_pop_fnh_all"]][["trace"]][["posterior"]][["p_N_h"]] %>%
  filter(setting == "yap") %>% .$value %>% mean
n_infected/N

##      2.5%      50%     97.5%
## 0.6820483 0.7246585 0.7699886

```

Reduced susceptibility against Zika in Yap

Generate MCMC chains

In this model, the population susceptible to Zika in Yap is reduced by a factor r .

Fit the model (remember to update code_dir and data_dir in dengue_zika_mcmc.r):

```

Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations

```

Get MCMC chains of the two libbi runs

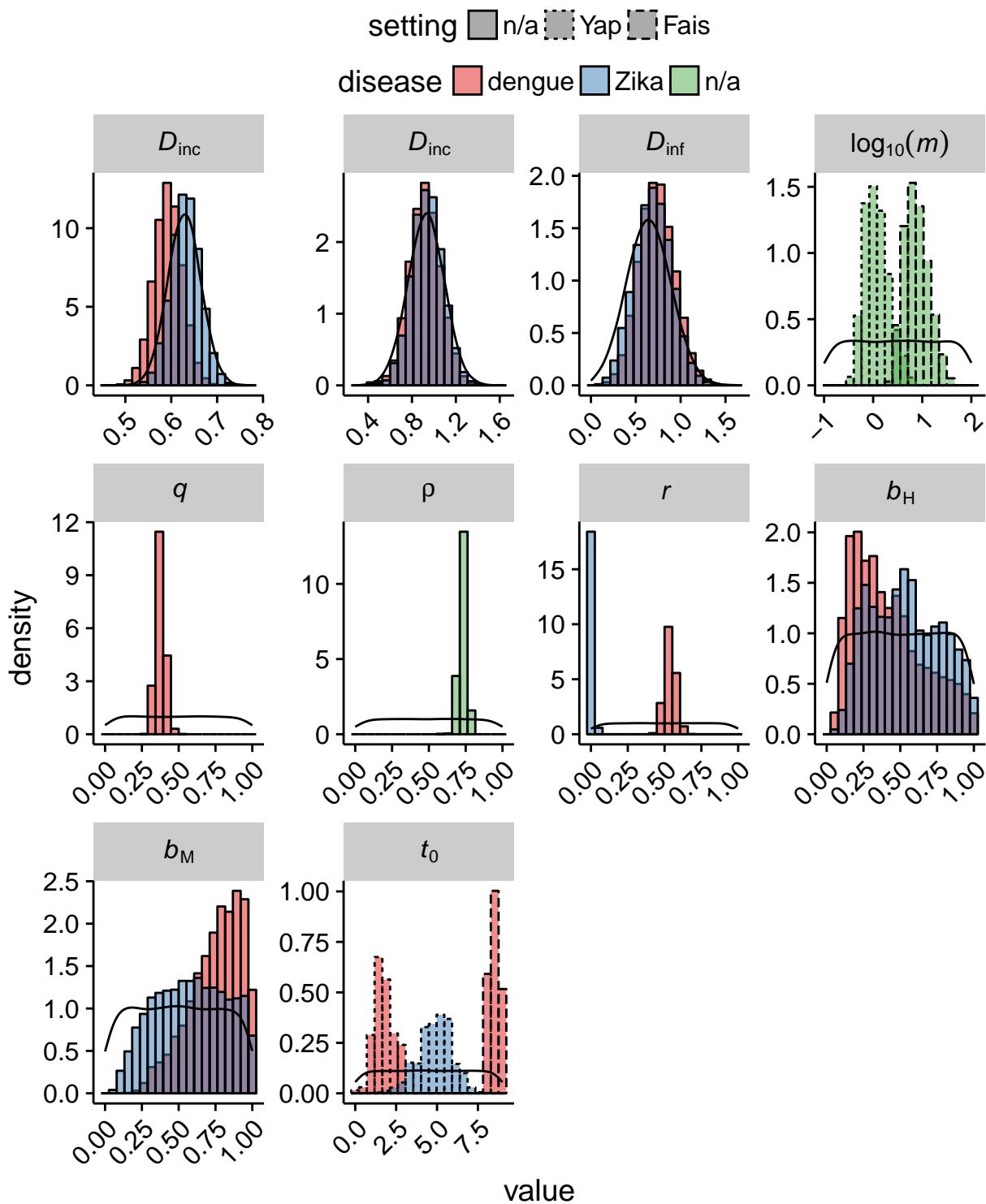
```
libbi_results <- analyse_traces(c("vbd_sero_fnh", "vbd_sero_fnh_shorter"), output_dir)
```

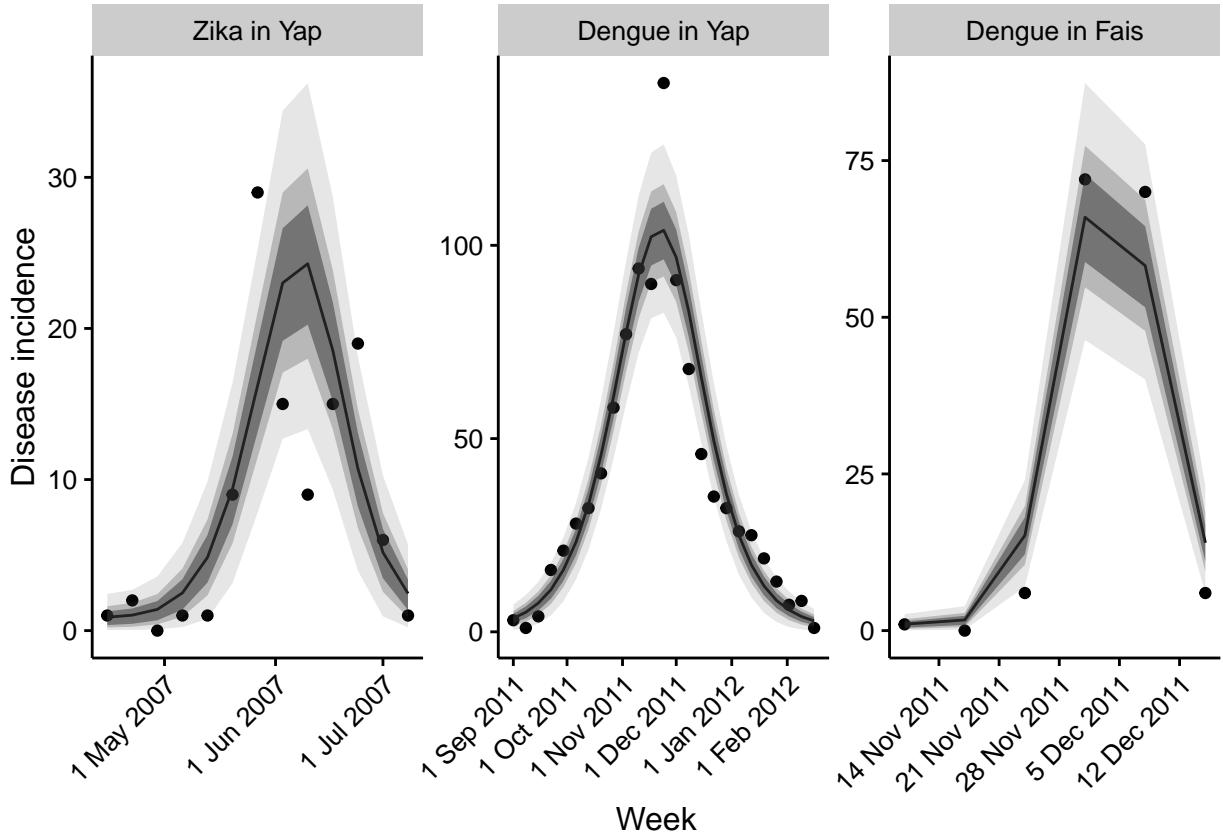
Fits

```

libbi_results[["vbd_sero_fnh_all"]][["trace"]][["posterior"]][["Cases"]] <- libbi_results[["vbd_sero_fnh_all"]][["trace"]][["posterior"]][["Cases"]]
  mutate(obs_id = factor(obs_id, levels = ordered_obs_id_levels, labels = data_labels))
temp_plot <- plot_libbi(read = libbi_results[["vbd_sero_fnh_all"]][["trace"]][["posterior"]][["Cases"]],
                         model = libbi_results[["vbd_sero_fnh_all"]][["model"]], data = data %>%
  filter(value > 0), density_args = list(adjust = 2), extra.aes = list(group = "obs_id"),
  data.colour = "black", states = "Cases", trend = "mean", plot = FALSE, limit.to.data = TRUE,
  quantiles = c(0.5, 0.72, 0.95))
obs_states <- temp_plot$data$states %>% inner_join(data %>% select(time, obs_id,
  onset_date), by = c("time", "obs_id"))
p_obs <- ggplot(obs_states, aes(x = onset_date)) + geom_point(data = data, mapping = aes(y = value)) +
  facet_wrap(~obs_id, scales = "free") + scale_x_date("Week", labels = scales::date_format("%e %b %Y"),
  theme_cowplot(font_size = 12) + theme(axis.text.x = element_text(angle = 45,
  hjust = 1)) + facet_wrap(~obs_id, scales = "free") + scale_y_continuous("Disease incidence") +
  geom_line(aes(y = value)) + geom_ribbon(aes(ymin = min.1, ymax = max.1),
  alpha = 0.5) + geom_ribbon(aes(ymin = min.2, ymax = max.2), alpha = 0.25) +
  geom_ribbon(aes(ymin = min.3, ymax = max.3), alpha = 0.125)

```





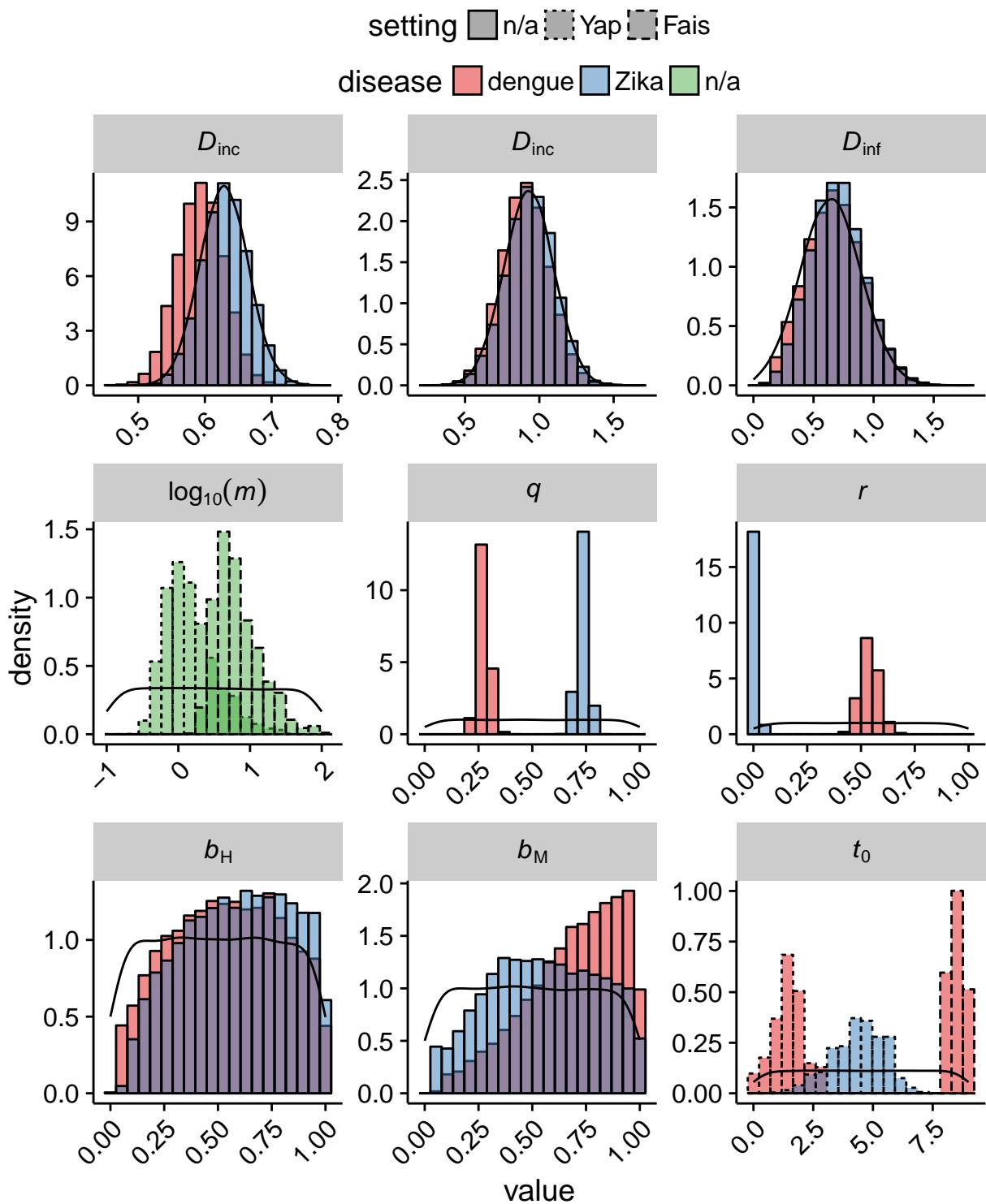
p_obs

Marginal posterior densities

```
p <- plot_libbi(read = libbi_results[["vbd_serofnh_all"]][["trace"]][["posterior"]],
                 prior = libbi_results[["vbd_serofnh_all"]][["trace"]][["prior"]],
                 model = libbi_results[["vbd_serofnh_all"]][["trace"]][["model"]],
                 density_args = list(bins = 20, alpha = 0.5, color = "black"),
                 densities = "histogram",
                 extra.aes = list(color = "disease", linetype = "setting"),
                 trend = "median",
                 plot = FALSE,
                 quantiles = c(0.5, 0.95),
                 labels = labels,
                 brewer.palette = "Set1")
p$densities
```

Estimated final size for Zika in Yap (proportion infected in the outbreak)

```
n_infected <- libbi_results[["vbd_serofnh_all"]][["trace"]][["posterior"]][["final_size"]]
N <- libbi_results[["vbd_serofnh_all"]][["trace"]][["posterior"]][["p_N_h"]]
n_infected/N
##          2.5%        50%       97.5%
## 0.6844271 0.7296974 0.7736204
```



Two-patch model

Fit the model (remember to update code_dir and data_dir in dengue_zika_mcmc.r):

```
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations  
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations
```

Get MCMC chains of the two libbi runs.

```
libbi_results <- analyse_traces(c("vbd_patch_fnh", "vbd_patch_fnh_shorter"),  
                                output_dir)
```

Fits

```
libbi_results[["vbd_patch_fnh_all"]][["trace"]][["posterior"]][["Cases"]] <- libbi_results[["vbd_patch_fnh_all"]]  
  mutate(obs_id = factor(obs_id, levels = ordered_obs_id_levels, labels = data_labels))  
temp_plot <- plot_libbi(read = libbi_results[["vbd_patch_fnh_all"]][["trace"]][["posterior"]][["Cases"]],  
  model = libbi_results[["vbd_patch_fnh_all"]][["model"]], data = data %>%  
  filter(value > 0), density_args = list(adjust = 2), extra.aes = list(group = "obs_id"),  
  data.colour = "black", states = "Cases", trend = "mean", plot = FALSE, limit.to.data = TRUE,  
  quantiles = c(0.5, 0.72, 0.95))  
obs_states <- temp_plot$data$states %>% inner_join(data %>% select(time, obs_id,  
  onset_date), by = c("time", "obs_id"))  
p_obs <- ggplot(obs_states, aes(x = onset_date)) + geom_point(data = data, mapping = aes(y = value)) +  
  facet_wrap(~obs_id, scales = "free") + scale_x_date("Week", labels = scales::date_format("%e %b %Y")) +  
  theme_cowplot(font_size = 12) + theme(axis.text.x = element_text(angle = 45,  
  hjust = 1)) + facet_wrap(~obs_id, scales = "free") + scale_y_continuous("Disease incidence") +  
  geom_line(aes(y = value)) + geom_ribbon(aes(ymin = min.1, ymax = max.1),  
  alpha = 0.5) + geom_ribbon(aes(ymin = min.2, ymax = max.2), alpha = 0.25) +  
  geom_ribbon(aes(ymin = min.3, ymax = max.3), alpha = 0.125)  
  
p_obs
```

Marginal posterior densities

```
p <- plot_libbi(read = libbi_results[["vbd_patch_fnh_all"]][["trace"]][["posterior"]],  
  prior = libbi_results[["vbd_patch_fnh_all"]][["trace"]][["prior"]], model = libbi_results[["vbd_patch_fnh_all"]][["prior"]],  
  density_args = list(bins = 20, alpha = 0.5, color = "black"), densities = "histogram",  
  extra.aes = list(color = "disease", linetype = "setting"), trend = "median",  
  plot = FALSE, quantiles = c(0.5, 0.95), labels = labels, brewer.palette = "Set1")  
p$densities
```

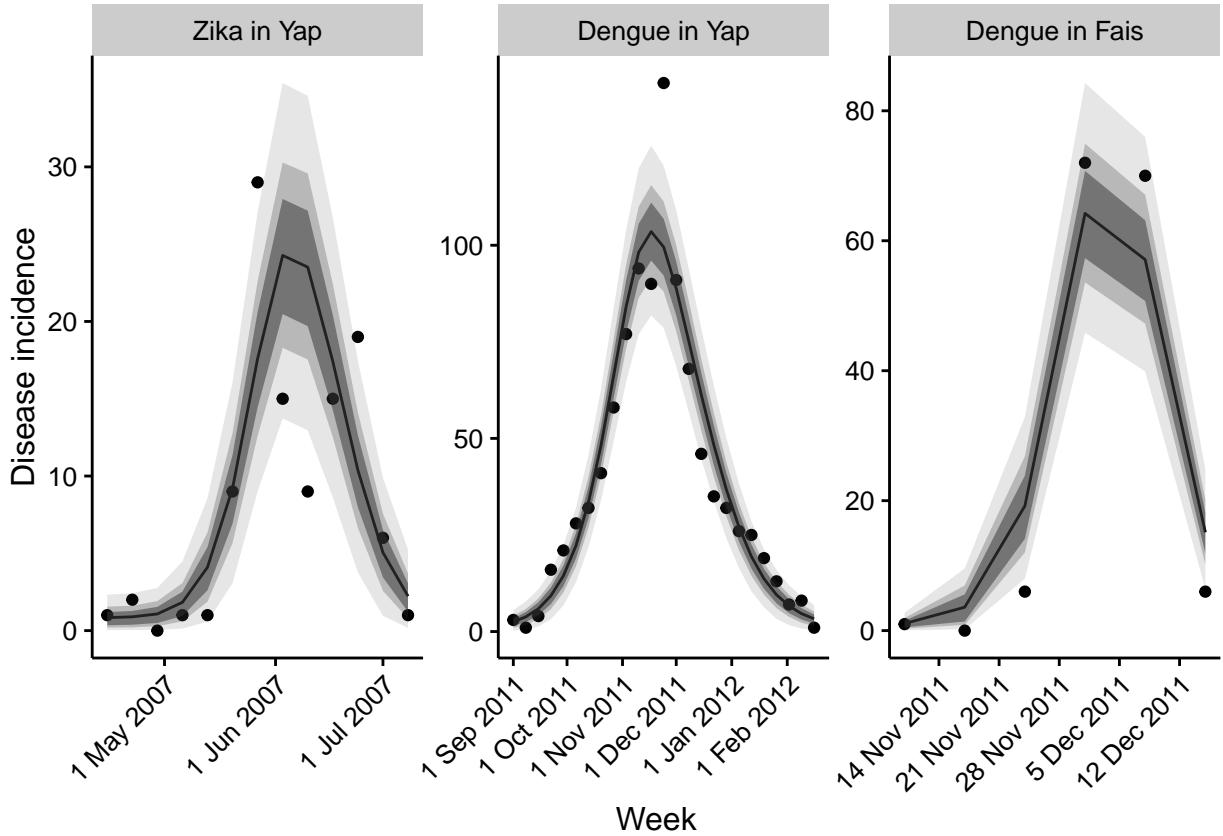
Fitting the Zika outbreak in Yap in isolation

Fit the model (remember to update code_dir and data_dir in dengue_zika_mcmc.r):

```
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations  
Rscript dengue_zika_mcmc.r --nsamples 10000000 --pre_samples 10000 --sample-prior --sample-observations
```

Get MCMC chains of the two libbi runs.

```
libbi_results <- analyse_traces(c("vbd_patch_fnh_yap_zika", "vbd_patch_fnh_shorter_yap_zika"),  
                                output_dir)
```



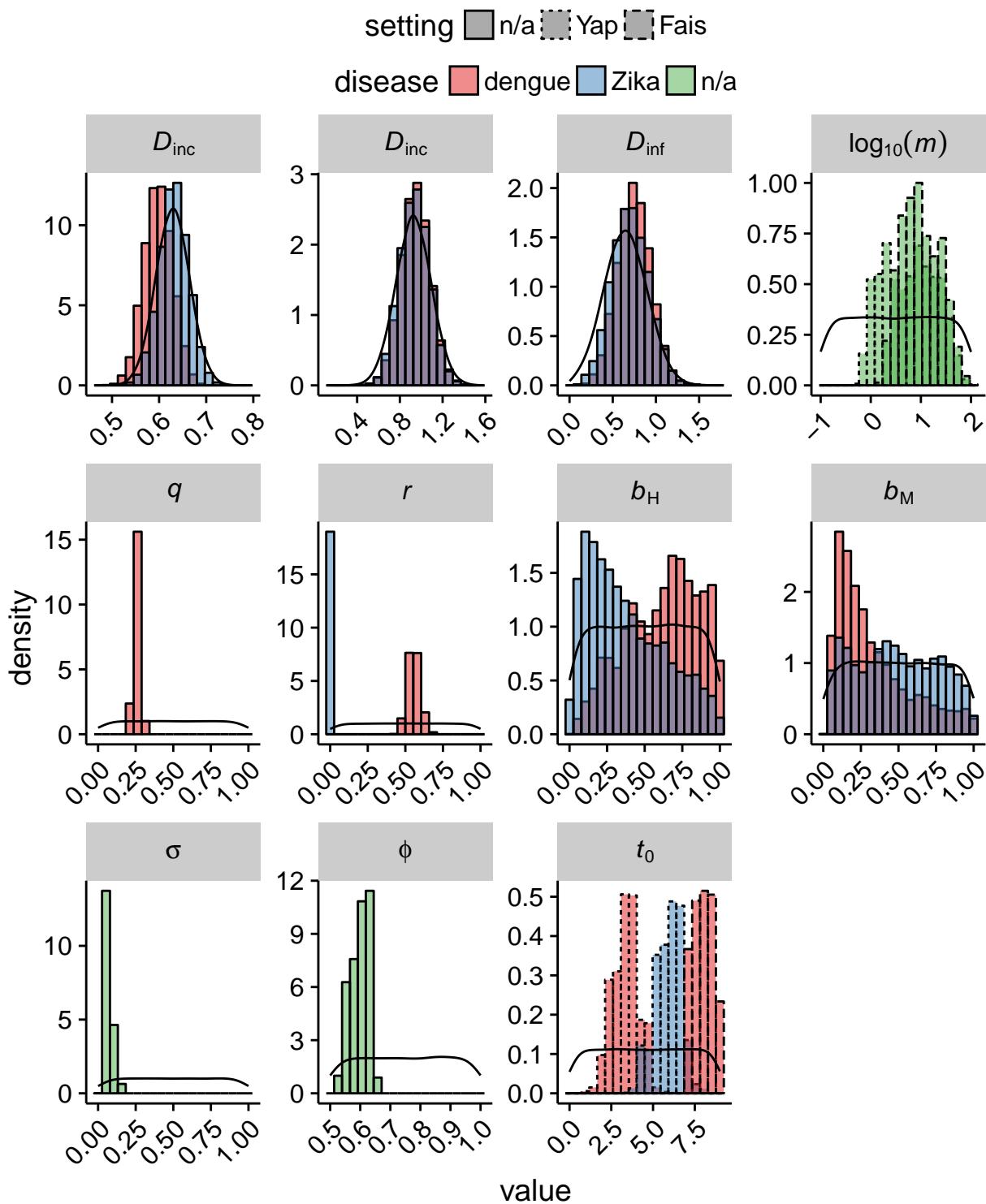
Fit

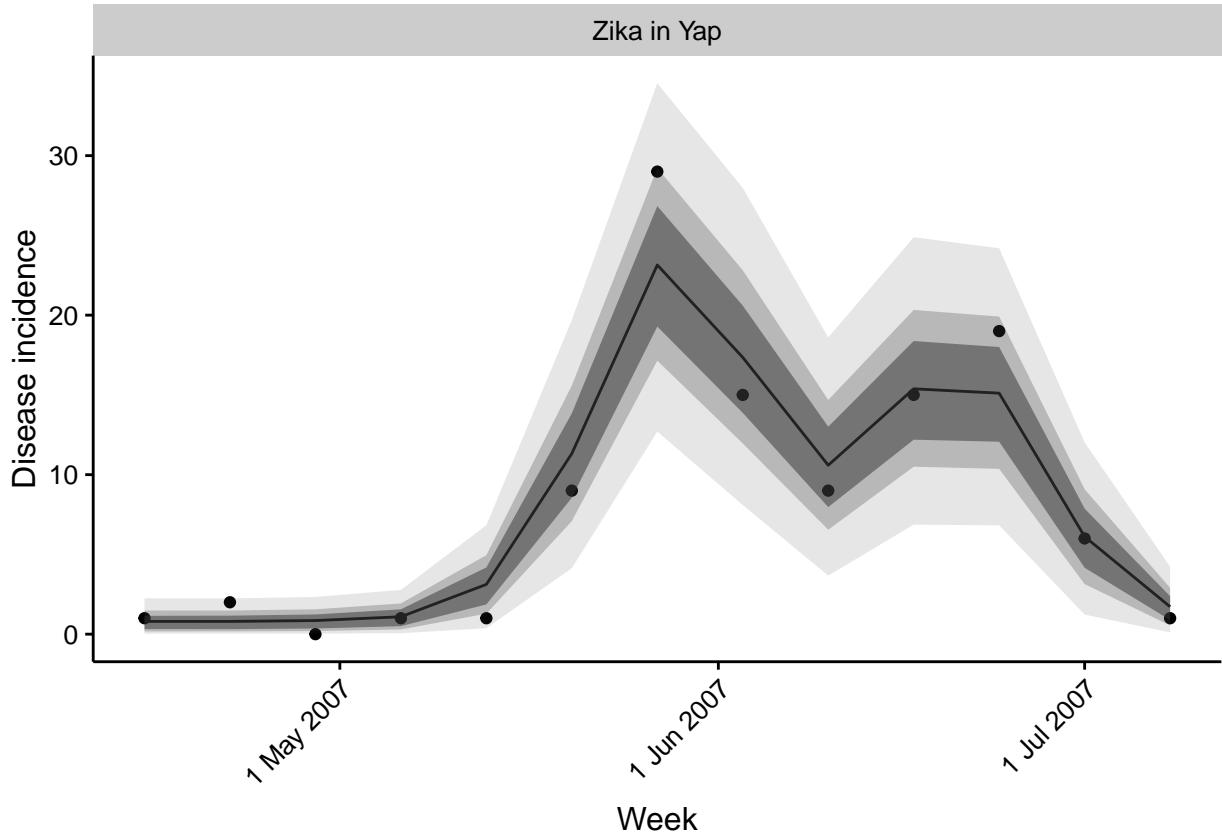
```
libbi_results[["vbd_patch_fnh_yap_zika_all"]][["trace"]][["posterior"]][["Cases"]] <- libbi_results[["vbd_patch_fnh_yap_zika_all"]]
  mutate(obs_id = factor(obs_id, levels = ordered_obs_id_levels, labels = data_labels))
temp_plot <- plot_libbi(read = libbi_results[["vbd_patch_fnh_yap_zika_all"]][["trace"]][["posterior"]][["Cases"]])
model = libbi_results[["vbd_patch_fnh_yap_zika_all"]][["model"]], data = data,
density_args = list(adjust = 2), extra.aes = list(group = "obs_id"), data.colour = "black",
states = "Cases", trend = "mean", plot = FALSE, limit.to.data = TRUE, quantiles = c(0.5,
0.72, 0.95))
obs_states <- temp_plot$data$states %>% inner_join(data %>% select(time, obs_id,
onset_date), by = c("time", "obs_id"))

p_obs <- ggplot(obs_states, aes(x = onset_date)) + geom_point(data = data %>%
filter(obs_id == "Zika in Yap"), mapping = aes(y = value)) + facet_wrap(~obs_id,
scales = "free") + scale_x_date("Week", labels = scales::date_format("%e %b %Y")) +
theme_cowplot(font_size = 12) + theme(axis.text.x = element_text(angle = 45,
hjust = 1)) + facet_wrap(~obs_id, scales = "free") + scale_y_continuous("Disease incidence") +
geom_line(aes(y = value)) + geom_ribbon(aes(ymin = min.1, ymax = max.1),
alpha = 0.5) + geom_ribbon(aes(ymin = min.2, ymax = max.2), alpha = 0.25) +
geom_ribbon(aes(ymin = min.3, ymax = max.3), alpha = 0.125)

p_obs
```

Marginal posterior densities





```

p <- plot_libbi(read = libbi_results[["vbd_patch_fnh_yap_zika_all"]][["trace"]][["posterior"]],  

  prior = libbi_results[["vbd_patch_fnh_yap_zika_all"]][["trace"]][["prior"]],  

  model = libbi_results[["vbd_patch_fnh_yap_zika_all"]][["model"]], density_args = list(bins = 20,  

    alpha = 0.5, color = "black"), densities = "histogram", extra.aes = list(color = "disease",  

    linetype = "setting"), trend = "median", plot = FALSE, quantiles = c(0.5,  

    0.95), labels = labels, brewer.palette = "Set1")  

p$densities

Human-to-human reproduction number vs generation interval

temp_plot <- plot_libbi(read = libbi_results[["vbd_patch_fnh_yap_zika_all"]][["trace"]][["posterior"]],  

  prior = libbi_results[["vbd_patch_fnh_yap_zika_all"]][["trace"]][["prior"]],  

  model = libbi_results[["vbd_patch_fnh_yap_zika_all"]][["model"]], extra.aes = list(color = "disease",  

    linetype = "setting", group = "p_d_life_m"), plot = FALSE, labels = labels,  

  states = c(), params = c("R0", "GI"), noises = c())  

r0gi <- temp_plot$data$params %>% filter(distribution == "posterior") %>% mutate(obs_id = tolower(pas-  

  disease, sep = "_")) %>% filter(obs_id != "fais_zika") %>% mutate(obs_id = factor(obs_id,  

  levels = ordered_obs_id_levels, labels = data_labels)) %>% spread(parameter,  

  value)  

p_r0vgi <- ggplot(r0gi, aes(x = `italic(G)` * 7)) + geom_jitter(aes(y = `italic(R)[H %->% H]`),  

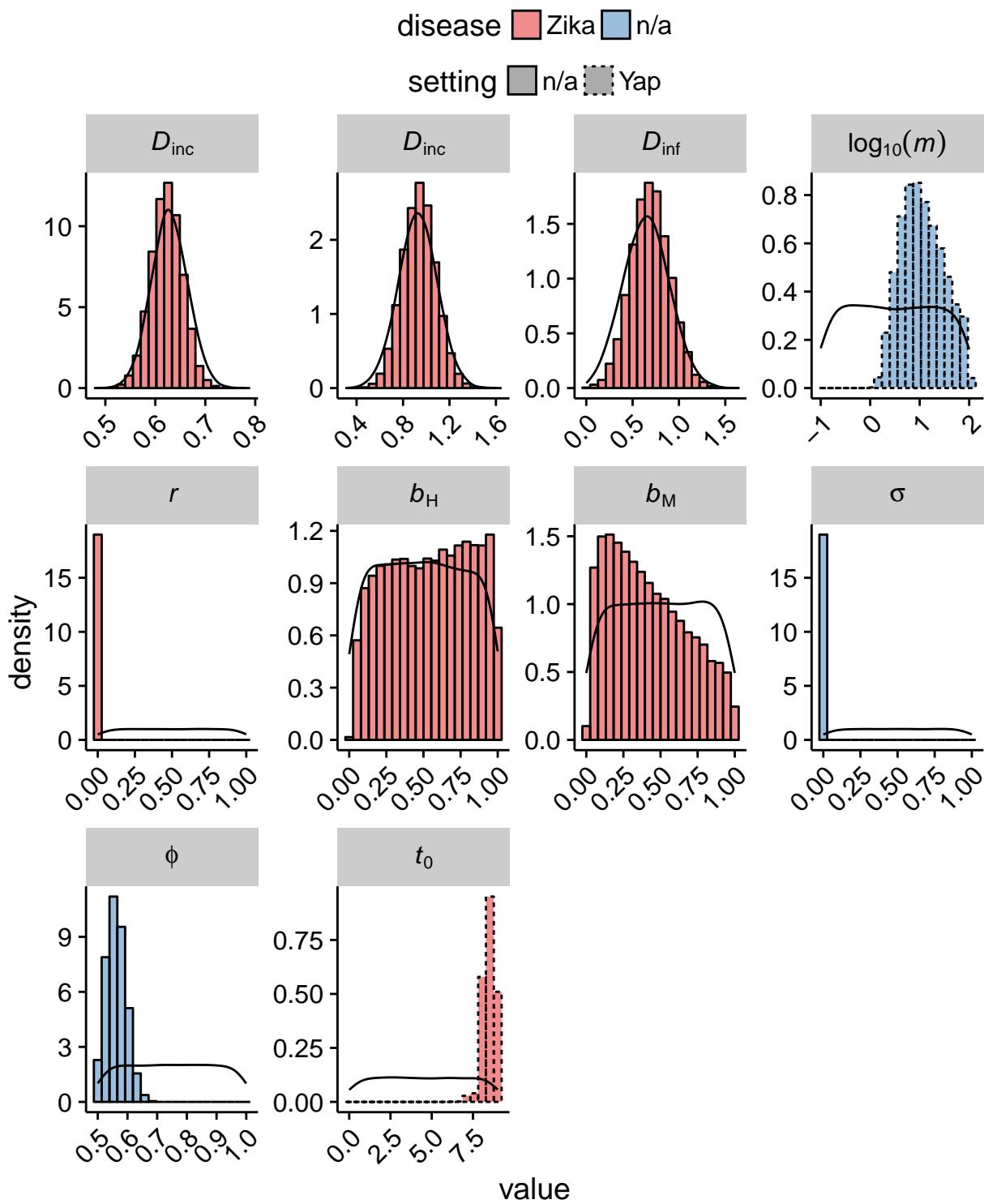
  color = factor(p_d_life_m)) + facet_grid(~obs_id) + scale_x_continuous("Equilibrium generation in",  

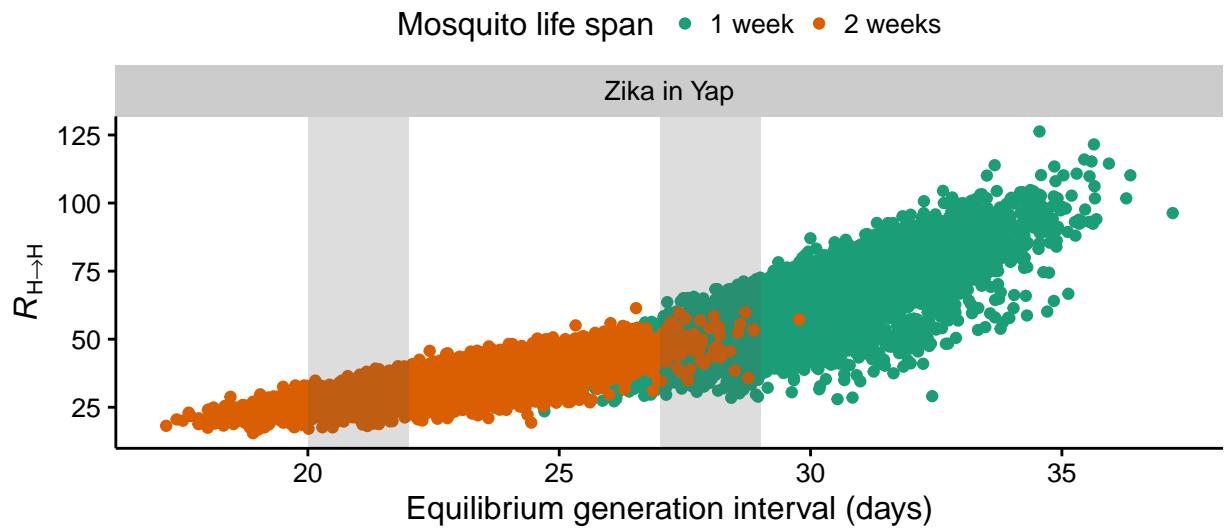
  scale_y_continuous(expression(italic(R)[H %->% H]))) + scale_color_brewer("Mosquito life span",  

  palette = "Dark2", labels = c("1 week", "2 weeks")) + theme_cowplot(font_size = 12) +  

  theme(legend.position = "top") + facet_wrap(~obs_id, scales = "free") +

```





```
geom_rect(data = cross_sections, aes(xmin = `italic(G)` * 7 - 1, xmax = `italic(G)` * 7 + 1), ymin = -Inf, ymax = Inf, alpha = 0.2, lwd = 3)
p_r0vgi
```